

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-033-223-1.res made by ehart on Wed 15 Jun 105 13:54:08-PST

Query sequence being compared: US-10-033-223-1 (1-1283)

Number of sequences searched:
Number of scores above cutoff:

Results of the initial comparison of US-10-033-223-1 (1-1283) with:
File : hsu31875.seq

Letter	Score (approx.)
N	95
U	85
M	75
B	65
E	55
R	45
O	35
F	25
S	15
S	10
E	5
O	5
U	5
E	5
N	5
C	5
E	5

PARAMETERS

	Unitary	K-tuple Joining penalty Window size
Similarity matrix	1	4
Mismatch penalty	5.00	30
Gap penalty	0.33	3
Gap size penalty	1	500
Cutoff score	0	
Randomization group		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	412	0	0.00
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00

Number of residues:	1442
Number of sequences searched:	1
Number of scores above cutoff:	1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

identical sequence to the query sequence was not found

of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame
1. hnu31875	TOIG of: hnu31875	check: 292	1442	412	621	0.00 0

1. US-10-033-223-1 (1-1283) check: 2920 from: 1 to: 1442
hsu31875 TOIG of: hsu31875

Initial Score	=	412	Optimized Score	=	621	Significance	=	0.00
Residue Identity	=	61%	Matches	=	642	Mismatches	=	372
Gaps	=	23	Conservative Substitutions	=			=	0

CGACGCGTGGACCCATCTT

CACCAAGCGGTGAGACTATCACCTATCGCCAAAGTGGCCTGATTCAGCAGGAAGCATCTAGACACCAACAC
370 380 390 400 410 420 430

GCTGATCGATCCATGACACAAGCGGGGCTGTAGGCCTGTGTGCCCGGCTTGAATTCCGTGCGAATGCG
30 40 50 60 70 80 90
TATCTGTCAAGACTTGCCCGGGGCTAACCAAGGCGGTTCATCCTCTGTGTAGGCTTCTGTGTGAAATGAG
440 450 460 470 480 490 500

[illegible]

170 180 190 200 210 220 230
CGGCTTCGCATCGCCGCGCTTTGGCCGAGACGAGGCCCATGTGCTCTCAGCAGCTGGTAGCGACGACAA
CGGCTTTCCATCGCCGACCTCTGCGCCGAGAGGAGGCCCACTGTATCAGACCGAAGCAGCAGAA
580 590 600 610 620 630 640

240
250
260
270
280
290
300
310
320
330
340
350
360
370
380
390
400
410
420
430
440
450
460
470
480
490
500
510
520
530
540
550
560
570
580
590
600
610
620
630
640
650
660
670
680
690
700
710
720

[illegible]

390 400 410 420 430 440 450
 TGTGCTGTCAACCTCTTTTGGAGCATTAATGATTCCTGAGGAGGTGGGACAAGATCTGGACA
 CGAGAGGCTCAACCTCTGTGTGAGGAGCATCTGGGAGCAGTGGAGCATCTGGACAAGATCTTAAAGTC
 800 810 820 830 840 850 860

460 470 480 490 500 510 520
TAATGGAAGCCCTCCAGCCCTTAATGCAAGGCACTGGTGCAGAAATGAGGAACAGAGAGGCTCA
GAACTGTAATCCCAAGCCCTGTGTGTGAGCAGTTGCTGCTTCAATGAGGAACAGAGGGGTG---CTC
870 880 890 900 910 920 930

530 540 550 560 570 580 590
GGTATGTCCTCCCATAGCAGACCTTAGTCAGTCACTCTCGCTTCAGTCCCTCAATGCAGTAACA
CATCTGTCTTCCATTGACGACTAATATCAGTAAGTGCGCTGGTGCTTAACTAGAAGCACAG

940 950 960 970 980 990 1000

600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800
CTTCTGAGGCTGACCAAGCCTTGCCATPAGGTGCGCCCAAGAAATTAGGGTGAATCTGCTGACCA
GCTCTGGGCTCACTGAAACATGCGATTGGAGCTGGCGCCCAAGACATCCGGTAACTGGGTGTTT
1010 1020 1030 1040 1050 1060 1070

-30M
Q217

680 690 700 710 720 730 740
TGGACTTATCAAGACTAGCTCAGCAGATGCTCTGATGGAAGAAGAAAGCATGAAGAAAC
AGGATTTTAAATACTGACTTCAAGAAATGTTTCAATGGAATGACTCTCTCTGAAAGACTTCAAGAAACA
1080 1090 1100 1110 1120 1130 1140
750 760 770 780 790 800 810
CCTGGGATTAAGAGATTAGCGGACCAAGAGATTGCTGCTGCTCTTCTCTGCTGGAAGATGC
TCATCAGCTGCAGAGATTGGGAGTCAAGAGACTGTGAGAAATGTCCTTCTGCTGCTCTCAAGATGC
1150 1160 1170 1180 1190 1200 1210 1220
820 830 840 850 860
CAGCTACATCACTGGGAAACAGTGTGTGTGAGAGAACCC-----GTCCGCGCT
CAGCTACGTCACGGGAGAACATTCGGGTGCAAGCTTCACTCGGCTCTGAGAGAGATGGGGCGGCT
1230 1240 1250 1260 1270 1280 1290
870 880 890 900 910 920 930 940
CTGAGAACCGGAGACAGCCCAAGGCCAGATTGGGCTCTAGCTCTGTGCTGCTCTGATTCACCCAC
GGTAGCTGTGTCAGGCCAGAGCCTGAGGGGTGTCTAGTATCATTTGAAATCG--AGCAGATC
1300 1310 1320 1330 1340 1350 1360
950 960 970 980 990 1000 1010
TGGCCTTCCCACTCTGTCTCACTTACTTCACTCAATCAATCAATTCAGTTCTGCCCTGTGAAAGATCCAGC
TGCATTTCTGCAGACTAGCAATTTGGGGCTTACTCATGCTTAGGCTTGAGAGAGAGAAACGCTTCGGC
1370 1380 1390 1400 1410 1420 1430
1020 1030 1040 1050 1060
CTTCCCTGCGGTCAGAGTGCCTCTTACTCGGGAATTCCTGCTGTGTGTGCGCTTG
ATTCTCC
1440 X